(HR=0.39; 95% CI 0.17-0.93, p=0.034) and OS (HR=0.32; 95% CI 0.12-0.82, p=0.017).

Conclusions: A high level of telomerase expression in tumoral tissue is strongly associated with increased risk of recurrence and mortality in resected NSCLC. The level of hTERT mRNA would predict the prognosis of lung cancer patients.

P2-084 **BSTB: Prognostic Factors Posters, Tue, Sept 4**

Prognostic value of atelectasis for locally advanced non-small cell lung cancer (NSCLC)

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Purpose: According to the TNM staging system, atelectasis (At) is considered a bad prognostic factor within the T category. According to our clinical experience we intuitively considered the opposite. The aim of the study was to evaluate the influence of atelectasis on patient outcome for unresectable stage III and IV (NSCLC).

Patients and Methods: We prospectively evaluated the median progression free (PFS) and overall survival (MS), for the patients with pathologically/ citologically proven NSCLC, in relation with the presence or absence of the atelectasis. The treatment consisted of sequential chemo-radiation for stage III and platinum based combination chemotherapy with palliative irradiation for stage IV (PS:0-1). A preplanned analysis according to stage was foreseen.

Results: a number of 1352 consecutively treated patients, during 1997-2004, were evaluated. Overall, we identified a number of 68 (5%) patients with atelectasis, 46/592 patients with stage III and 22/760 stage IV, ratio sex M/F: 1108 (82%)/172 (17.5%), age range 23-82 (median age 57 years), histology: adenocarcinoma: 419 (31%), squamous cell: 327 (24%), undifferentiated: 127 (9.5%), other types: 31 (2.5%) and cytology: 448 (33%).

The median PFS and OS for patients with and without atelectasis are presented in table below.

		No. Pat.	PFS (m)	p	OS (m)	p	2ys Sv
			95% CI		95% CI		
St III (592)	At +	46	19	.0001	24	.0001	57%
(43.7%)			(11.22-25.78)		(18.65-29.35)		
	At -	546	8		14		13.5%
			(6.98-9.02)		(12.43-15.57)		
St IV (760)	At +	22	8	.1046	16	.1451	19%
(56.3%)			(5.80-10.20)		(4.49-27.51)		
	At -	738	6		9		4%
			(5.53 -6.47)		(8.61-9.39)		
Total	At +	68	16	<.0001	21		38%
			(11.19-20.81)		(12.37-29.63)		
	At -	1284	7		10		9.5%
			(6.53-7.47)		(9.48-10.52)		

Conclusion: Atelectasis predicts for better PFS and OS in patients with advanced NSCLC. The subset analysis showed a statistically significant improved PFS and OS for unresectable stage III. For stage IV there is also a trend towards improved survival but statistically not significant. The biologic impact of this clinical aspect in NSCLC should be further evaluated.

The multivariate analysis (including, age, sex, histology, RT, stage, type of chemotherapy) showed a statistically significant independent prognostic value for atelectasis for stage III, but not in stage IV.

P2-085 **BSTB: Prognostic Factors Posters, Tue, Sept 4**

Aberrant methylation of RASSF1A in small-sized lung adenocarcinoma and its relationship to clinicopathological features

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Purpose: Aberrant methylation of CpG islands in promoter regions of tumor cells is one of the major mechanisms for silencing of tumor suppressor genes. Chromosome 3p is deleted frequently in lung cancer. The RAS association domain family 1A (RASSF1A) gene was isolated from the 3p21.3 region homozygously deleted in lung cancer cell lines, and it was shown to be inactivated by hypermethylation of the promoter region in lung cancers. In this study, we investigated the clinicopathological significances of RASSF1A methylation in the development and/or progression of small-sized (less than 2.0cm) lung adenocarcinoma. It is important to identify a marker for high-risk early stage patients who should benefit from new investigational adjuvant therapies.

Methods: Surgically resected specimens from 260 primary lung adenocarcinoma 77 cases of small-sized adenocarcinoma. We determined the frequency of aberrant promoter methylation of the RASSF1A genes in 77 small-sized lung adenocarcinoma. Aberrant promoter methylation was examined using methylation-specific PCR (MSP).

Results: Twenty-five of 77 (32.5%) tumors showed RASSF1A methylation. RASSF1A methylation was dominantly detected in smoker ($p<0.03$). There was no significant correlation of RASSF1A methylation with gender, age, T stage, N stage and pathological stage. RASSF1A methylation correlated with adverse survival by univariate analysis ($p<0.005$; log-rank test) as well as multivariate analysis (p=0.0062; risk ratio 4.251; 95% confidence interval, 1.507-11.993). Furthermore, RASSF1A promoter hypermethylation in resected stage I small-sized lung adenocarcinoma was associated with impaired patient survival ($p<0.01$).

Conclusion: Aberrant promoter methylation of the RASSF1A was present in 25 of 77 (32.5%) of small-sized lung adenocarcinoma by MSP assay. These results indicated that epigenetic inactivation of RASSF1A plays an important role in the progression of small-sized lung adenocarcinoma, and that RASSF1A hypermethylation appears to be a useful molecular marker for the prognosis of patients with small-sized and stage I lung adenocarcinoma.

Clinical Implications: RASSF1A is a potential tumor suppressor gene that undergoes epigenetic inactivation in lung adenocarcinoma through hypermethylation of its promoter region. RASSF1A methylation was significantly related to unfavorable prognosis in small-sized lung adenocarcinoma.